SCIENCE CHINA
Life Sciences

• INSIGHT •

July 2012 Vol.55 No.7: 649–650
doi: 10.1007/s11427-012-4342-7

Recent progress in microRNA study: Benefits from technique advance

YU Jia* & WANG Fang

Department of Biochemistry and Molecular Biology, National Laboratory of Medical Molecular Biology, Peking Union Medical College & Chinese Academy of Medical Sciences, Beijing 100005, China

Received June 7, 2012; accepted June 23, 2012

Citation: Yu J, Wang F. Recent progress in microRNA study: Benefits from technique advance. Sci China Life Sci, 2012, 55: 649−650, doi: 10.1007/s11427-012-4342-7

Over the last decade, sequencing of different genomes revealed that an increase in organismal complexity is not merely explained by a dramatic increase in the number of protein-coding genes. However, the gradual increase in protein diversity contributes a lot to the complexity of higher organisms [1]. It is now widely accepted that non-coding RNAs (ncRNAs), especially microRNAs (miRNAs) largely define eukaryotic cell functions and the impacts of a variety of gene regulation [2].

As the first step, the identification and functional annotation of miRNAs are extremely important for elucidating miRNA biology. From then on, microchip [3], microarray [4,5] and RNA-Seq technology [6] have been widely used in miRNA gene identification, expression profile establishment and function investigation. Recently, the combination of some computational approach to experimental techniques makes miRNA research more convenient [7–9]. For example, numerous ncRNA databases, such as *RNAdb* [10], NONCODE [11], deepBase [12], miRBase [13], and Rfam [14], facilitate the usage of transcript information by miRNA researchers. A number of ncRNA gene prediction algorithms were also developed for the large-scale identification of new miRNAs [15–17]. The final purpose of identifying ncRNA genes is to reveal their function. ncRNAs often serve their roles by interacting with other molecules, therefore a series of algorithms were established to find target molecules, especially for miRNAs, such as *miRanda* [18], *TargetScan* [19], *PicTar* [20], and *RNAhybrid* [21].

Recently, the miRNA research also benefits from large progress in synthetic biology, e.g., a sensor for miRNA, which carried miRNA target sequences downstream to the 3′-untranslated region of Gaussia princeps luciferase (Gluc) gene, was developed to monitor *in vivo* miRNA activity in cell supernatants and peripheral blood [22].

Based on the above technique advances, some miRNAs and their functions in different species, including rats [23], tomatoes [24] and viruses [4,25], and in different human diseases, including acute myeloid leukemia [26], uveal melanoma [6], atrial fibrillation [27] and neurodegenerative diseases [5], have been well studied. These disclosed miRNAs may help promote the diagnosis of specific disease, and may be useful in developing therapies targeting miRNAs.

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*Corresponding author (email: j-yu@ibms.pumc.edu.cn)

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